

Fig. 1A

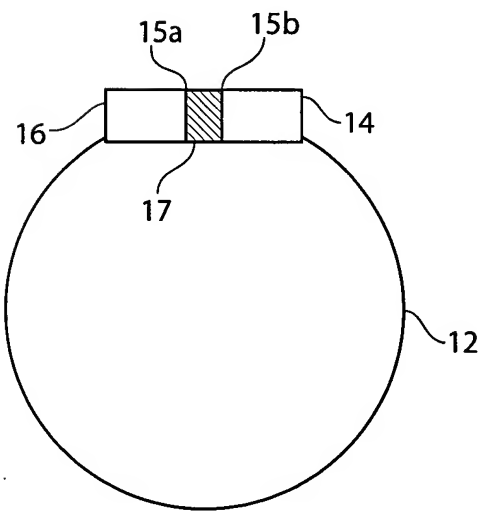


Fig. 1B

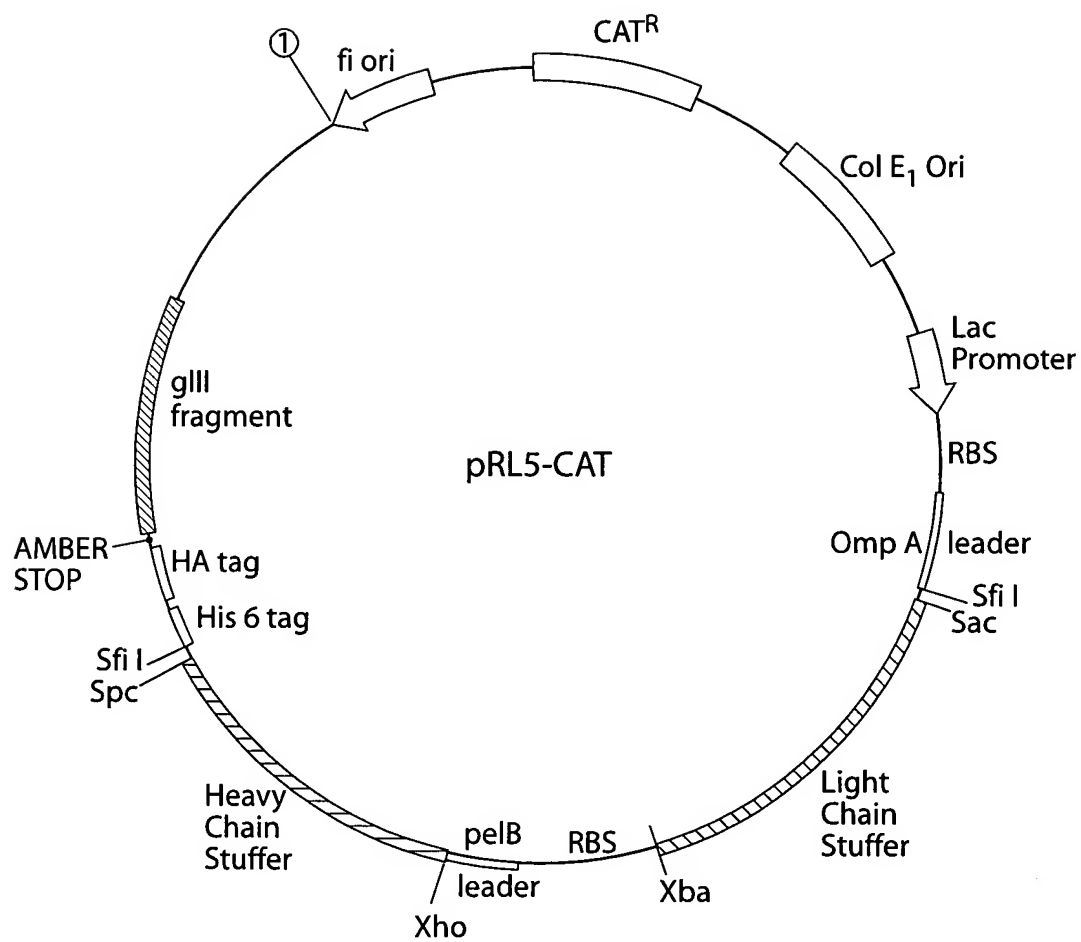


Fig. 2

PRL5-CAT

5' GGGAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTGT
AATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAATCCCTTATAAAT
CAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAG
TCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTAT
CAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTC
GAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCGATTTAGA
GCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGC
GAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACCGCTGCGCGT
AACCACCACACCCGCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGC
ACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACA
TTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAAT
ATTGAAAAGGAAGAGTATGAGTATTCACATTTCCGTGTCGCCCTTATTCCC
TTTTTTGCGGCATTTTGCCTTCCTGTTTTGCTCACCCAGAAACGCTGGTGAAA
GTAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAACTGG
ATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCA
ATGATGAGCACTTTTCGACCGAATAAATACCTGTGACGGAAGATCACTTCGC
AGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAAC
TTTTGGCGAAAATGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCACC
ATAATGAAATAAGATCACTACCGGGCGTATTTTTTTGAGTTGTGAGATTTTCA
GGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATAACCACCGTT
GATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGC
TCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGA
CCGTAAAGAAAAATAAGCACAGTTTTATCCGGCCTTTATTACATTCTTGCC
CGCCTGATGAATGCTCATCCGGAATTACGTATGGCAATGAAAGACGGTGAGC
TGGTGATATGGGATAGTGTTACCCCTTGTTACACCGTTTTCCATGAGCAAAC
GAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCT
ACACATATATTTCGAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCC
CTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGT
TTCACCAGTTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGT
TTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTG
GCGATTCAGGTTTCATCATGCCGTTTGTGATGGCTTCCATGTCGGCAGAAATGCT
TAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTT
TAAGGCAGTTATTGGTGCCCTTAAACGCCTGGTTGCTACGCCTGAATAAGTGA
TAATAAGCGGATGAATGGCAGAAATTCGAAAGCAAATTCGACCCGGTCGTCG
GTTACAGGGCAGGGTCGTAAATAGCCGCTTATGTCTATTGCTGGTTTACCGGT
TTATTGACTACCGGAAGCAGTGTGACCGTGTGCTTCTCAAATGCCTGAGGCCA
GTTTGCTCAGGCTCTCCCCGTGGAGGTAATAATTGACGATATGATCCTTTTTT
TCTGATCAAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAA
ATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGAT
CAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAA
CAAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACC
AACTCTTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATACT
GTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACC
GCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCG

Fig. 3A

ATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGC
 GCAGCGGTGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGA
 ACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCA
 CGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTGC
 GAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTT
 ATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGC
 TCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTAC
 GGTTCTTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTCTGCGTATCCC
 CTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGC
 CGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAG
 CGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCA
 GCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAAT
 TAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTC
 CGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTGAATTCAGGAGG
 AATTTAAATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTT
 CGCTACCGTGGCCAGGCGGCCGAGCTCGACTGCACTGGATGGTGGCGCTGG
 ATGGTAAGCCGCTGGCAAGCGGTGAAGTGCCTCTGGATGTCGCTCCACAAGG
 TAAACAGTTGATTGAACTGCCTGAACTACCGCAGCCGGAGAGCGCCGGGCAA
 CTCTGGCTCACAGTACGCGTAGTGCAACCGAACGCGACCGCATGGTCAGAAG
 CCGGGCACATCAGCGCCTGGCAGCAGTGGCGTCTGGCGGAAAACCTCAGTGT
 GACGCTCCCCGCCGCGTCCACGCCATCCCGCATCTGACCACCAGCGAAATG
 GATTTTTGCATCGAGCTGGGTAATAAGCGTTGGCAATTTAACCGCCAGTCAG
 GCTTCTTTCACAGATGTGGATTGGCGATAAAAAACAACCTGCTGACGCCGCT
 GCGCGATCAGTTCACCCGTGCACCGCTGGATAACGACATTGGCGTAAGTGAA
 GCGACCCGCATTGACCCTAACGCCTGGGTGCAACGCTGGAAGGCGGCGGGCC
 ATTACCAGGCCGAAGCAGCGTTGTTGCAGTGCACGGCAGATACACTTGCTGA
 TGCGGTGCTGATTACGACCGCTCACGCGTGGCAGCATCAGGGGAAAACCTTA
 TTTATCAGCCGGAAAACCTACCGGATTGATGGTAGTGGTCAAATGGCGATTA
 CCGTTGATGTTGAAGTGGCGAGCGATACACCGCATCCGGCGCGGATTGGCCT
 GAACTGCCAGCTGGCGCAGGTAGCAGAGCGGGTAACTGGCTCGGATTAGG
 GCCGCAAGAAAACCTATCCCGACCGCCTTACTGCCGCTGTTTTGACCGCTGGG
 ATCTGCCATTGTCAGACATGTATACTGGCTGCACCATCTGTCTTCATCTTCCC
 GCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGA
 ATAACCTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
 CCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAG
 CACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAA
 CACAAAGTATATGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCA
 CAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGA
 ATTTAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCG
 CTGCCCAACCAGCCATGGCCCTCGAGCTGATGAGCCATGGAAGCTGTGTGCG
 CTGCACCAGGCTCCACGGCTCGTGGTGGCGTGGCGCTTCTGGTGTTGCTGCC
 TACAGCCGACACGTCGAGCTTCTGTGCCCTAGAGTTGCGCGTCACAGCAGCC
 TCCGGCGCTCCGCGATATCACCGTGTCTACATCAATGAAGTAGTGCTCCT
 AGACGCCCCCGTGGGGCTGGTGGCGCGGTTGGCTGACGAGAGCGGCCACGTA
 GTGTTGCGCTGGCTCCCGCCGCCTGAGACACCCATGACGTCTCACATCCGCTA
 CGAGGTGGACGTCTCGGCCGGCAACGGCGCAGGGAGCGTACAGAGGGTGA

Fig. 3B

GATCCTGGAGGGCCGCACCGAGTGTGTGCTGAGCAACCTGCGGGGCGGACG
 CGCTACACCTTCGCCGTCCGCGCGCGTATGGCTGAGCCGAGCTTCGGCGGCTT
 CTGGAGCGCCTGGTCGGAGCCTGTGTGCTGCTGACGCCTAGCGACCTGGAC
 CCCCTCATCCTGACGCTCTCCCTCATCCTCGTGGTCATCCTGGTGCTGCTGAC
 CGTGCTCGCGCTGCTCTCCACCGCCGGGCTCTGAAGCAGAAGATCTGGCCT
 GGCATCCCGAGCCCAGAGAGCGAGTTTGAAGGCCTCTTCACCACCCACAAGG
 GTAACCTTCAGCTGTGGCTGTACCAGAATGATGGCTGCCTGTGGTGGAGCCC
 CTGCACCCCCCTTCACGGAGGACCCACCTGCTTCCCTGGAAGTCCTCTCAGAGC
 GCTGCTGGGGGACGATGCAGGCAGTGGAGCCGGGGACAGATGATGAGGGCC
 CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
 GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCG
 TGGAACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCCTAC
 AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG
 CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAAGTAGTGCCAG
 GCCGGCCAGCACCATCACCATCACCATGGCGCATACCCGTACGACGTTCCGG
 ACTACGCTTCTTAGGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGG
 CGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATT
 ATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCGAAAATGCCGATG
 AAAACGCGCTACAGTCTGACGCTAAAGGCAAACCTTGATTCTGTCGCTACTGA
 TTACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATG
 GTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTC
 GGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTC
 CCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTAGCGCTGGTAAACCAT
 ATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTTGCG
 TTTCTTTTATATGTTGCCACCTTTATGTATGTATTTTCTACGTTTGCTAACATA
 CTGCGTAATAAGGAGTCTTAAGCTAGCTAATTAATTTAAGCGGCCGCAGATC
 T3'

Fig. 3C

(SEQ. ID No. 1)

Ssp I
|

GGGAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTGTAAATCAGC
|....|....|....|....|....|....|....|....|....|....|.... 59

Psi I
|

TCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGAC
 |....|....|....|....|....|....|....|....|....|....|....|.... 118

CGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGG
 .|....|....|....|....|....|....|....|....|....|....|....|.. 177

Drd I
|

Ade I
Dra III
|

ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCA
 ..|....|....|....|....|....|....|....|....|....|....|....|.. 236

TCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAA
 ...|....|....|....|....|....|....|....|....|....|....|....|.... 295

NgoM IV
|

Nae I
|

AGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAG
|....|....|....|....|....|....|....|....|....|....|....|.... 354

BsrB I
Mbi I
|

GGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGC
 |....|....|....|....|....|....|....|....|....|....|....|.... 413

Fig. 4A

GTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTT
 .|...|...|...|...|...|...|...|...|...|...|...|...|.. 472

TCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGT
 ..|...|...|...|...|...|...|...|...|...|...|...|...|. 531

BsrB I
 Mbi I
 BspH I
 Bci VI
 Ssp I
 Ear I
 ATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGT
 ...|...|...|...|...|...|...|...|...|...|...|...|...|. 590

ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCC
|...|...|...|...|...|...|...|...|...|...|...|...|. 649

_____ Amp frag _____

Alw44 I
 ApaL I
 TGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTG
 |...|...|...|...|...|...|...|...|...|...|...|...|. 708

_____ Amp frag _____

BssS I
 Eco57 I
 CACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGC
 .|...|...|...|...|...|...|...|...|...|...|...|...|. 767

_____ Amp frag _____

Fig. 4B

Aci II
Xmn I

CCCGAAGAACGTTTTTCCAATGATGAGCACTTTTCGACCGAATAAATACCTGTGACGGAA
..|...|...|...|...|...|...|...|...|...|...|...|. 826

Amp frag

GATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGAAGCCCTGGGC
...|...|...|...|...|...|...|...|...|...|...|...|. 885

BsmB I
Van91 I Esp3 I

CAACTTTTGCGGAAAATGAGACGTTGATCGGCACGTAAGAGGTTCCAACTTTCACCATA
....|...|...|...|...|...|...|...|...|...|...|...|. 944

Bpu10 I

ATGAAATAAGATCACTACCGGGCGTATTTTTTGGAGTTGTGCGAGATTTTCAGGAGCTAAG
|...|...|...|...|...|...|...|...|...|...|...|...|. 1003

GAAGCTAAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCA
. |...|...|...|...|...|...|...|...|...|...|...|...|. 1062

Chloramphenicol transferase

TCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCG
..|...|...|...|...|...|...|...|...|...|...|...|. 1121

Chloramphenicol transferase

Fig. 4C

9/29

Pvu II Dra I

| |

TTCAGCTGGATATTACGGCCTTTTAAAGACCGTAAGGAAAAATAAGCACAAAGTTTTAT
...|...|...|...|...|...|...|...|...|...|...|...|...| 1180

Chloramphenicol transferase

BsaM I
 |
 Acc III
 |
 SnaB I
 |
 CCGGCCTTTATTACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTACGTATGGC
|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|..... 1239

Chloramphenicol transferase

BseMI
 BsrDI
 |
 AATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTACACCTTGTTACACCGTTTTCC
 |...|...|...|...|...|...|...|...|...|...|...|...|... 1298

Chloramphenicol transferase

[illegible]

Chloramphenicol transferase

TTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCC
 ..|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. 1416

Chloramphenicol transferase

Fig. 4D

10/29

BsmB I
 Esp3 I Van91 I
 | |
 TAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCA
 ...|...|...|...|...|...|...|...|...|...|...|...|...| 1475

Chloramphenicol transferase

Bal I
Dra I Msc I Bsp19 I
Nco I

GTTTTGATTTAACGTTGCCAATATGCACAACCTTCTTCGCCCCCGTTTTCCACCATGGGC
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|..... 1534

Chloramphenicol transferase

Ssp I
|
AAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTTCATCATGC
|...|...|...|...|...|...|...|...|...|...|...|...|... 1593

Chloramphenicol transferase

[illegible]

_____ Chloramphenicol transferase _____

AGTGGCAGGGCGGGCGTAATTTTTTAAAGGCAGTTATTGGTGCCCTTAAACGCCTGGT
 ..|.|.|.|.|.|.|.|.|.|.|.|. 1711

Fig.4E

11/29

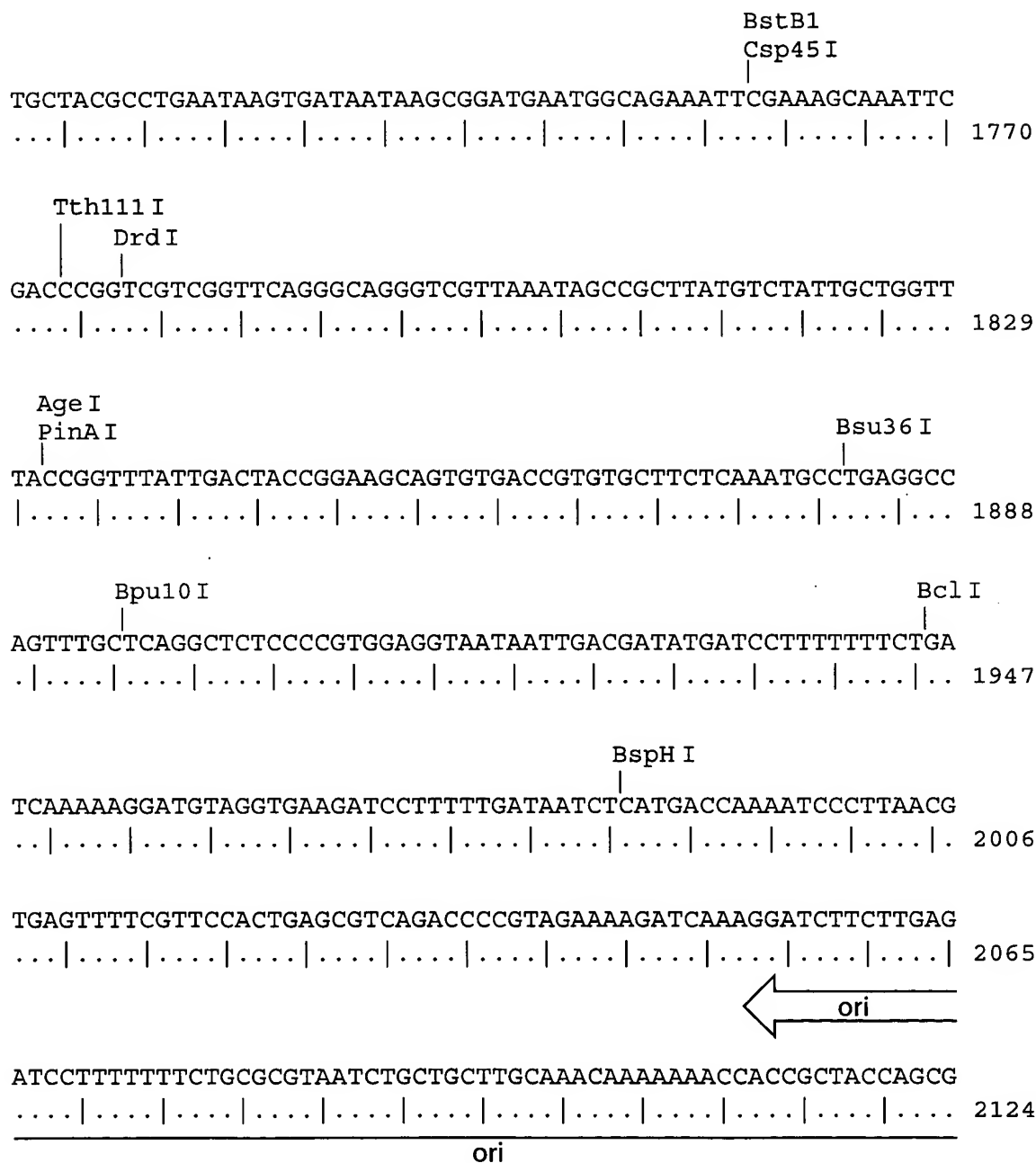


Fig. 4F

12/29

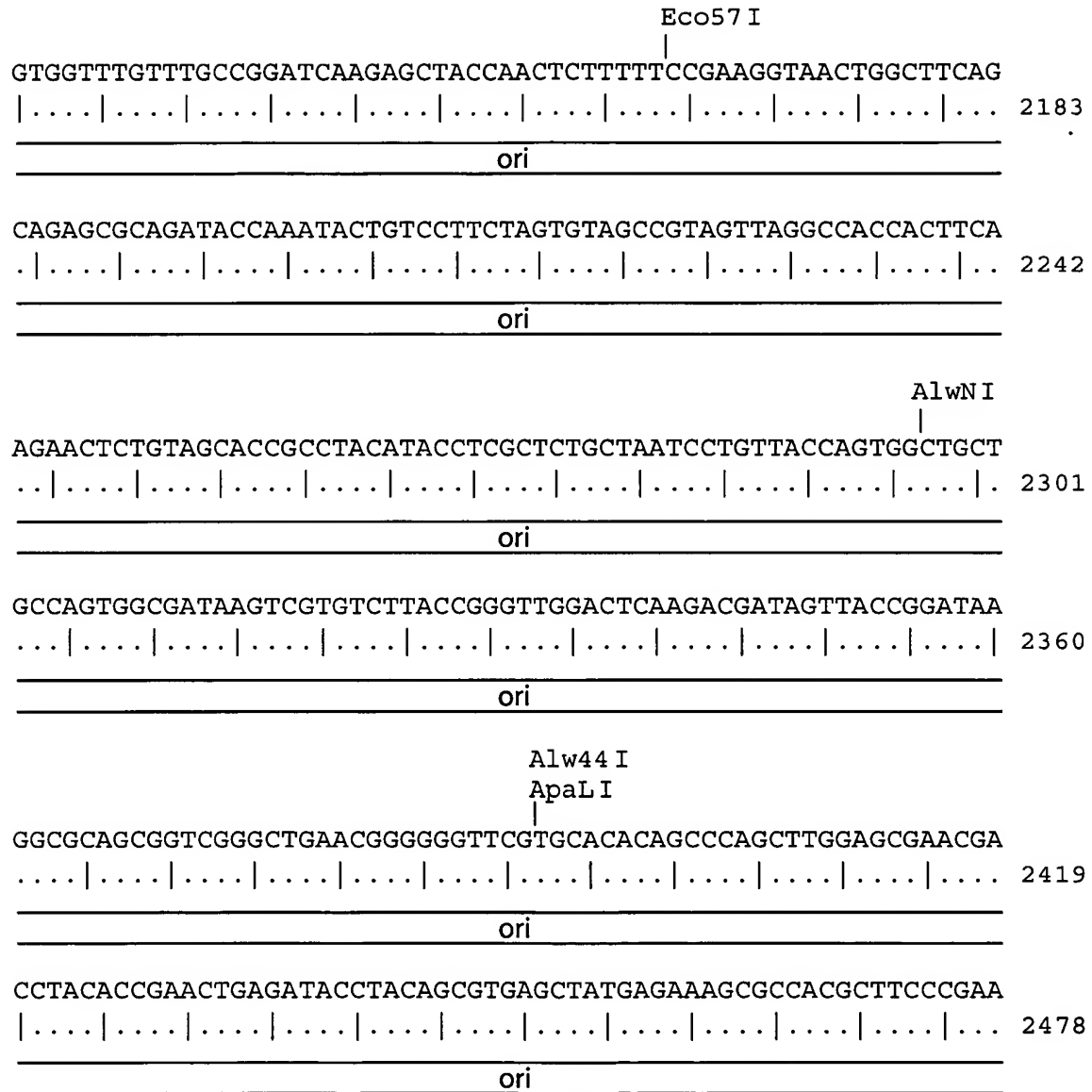


Fig. 4G

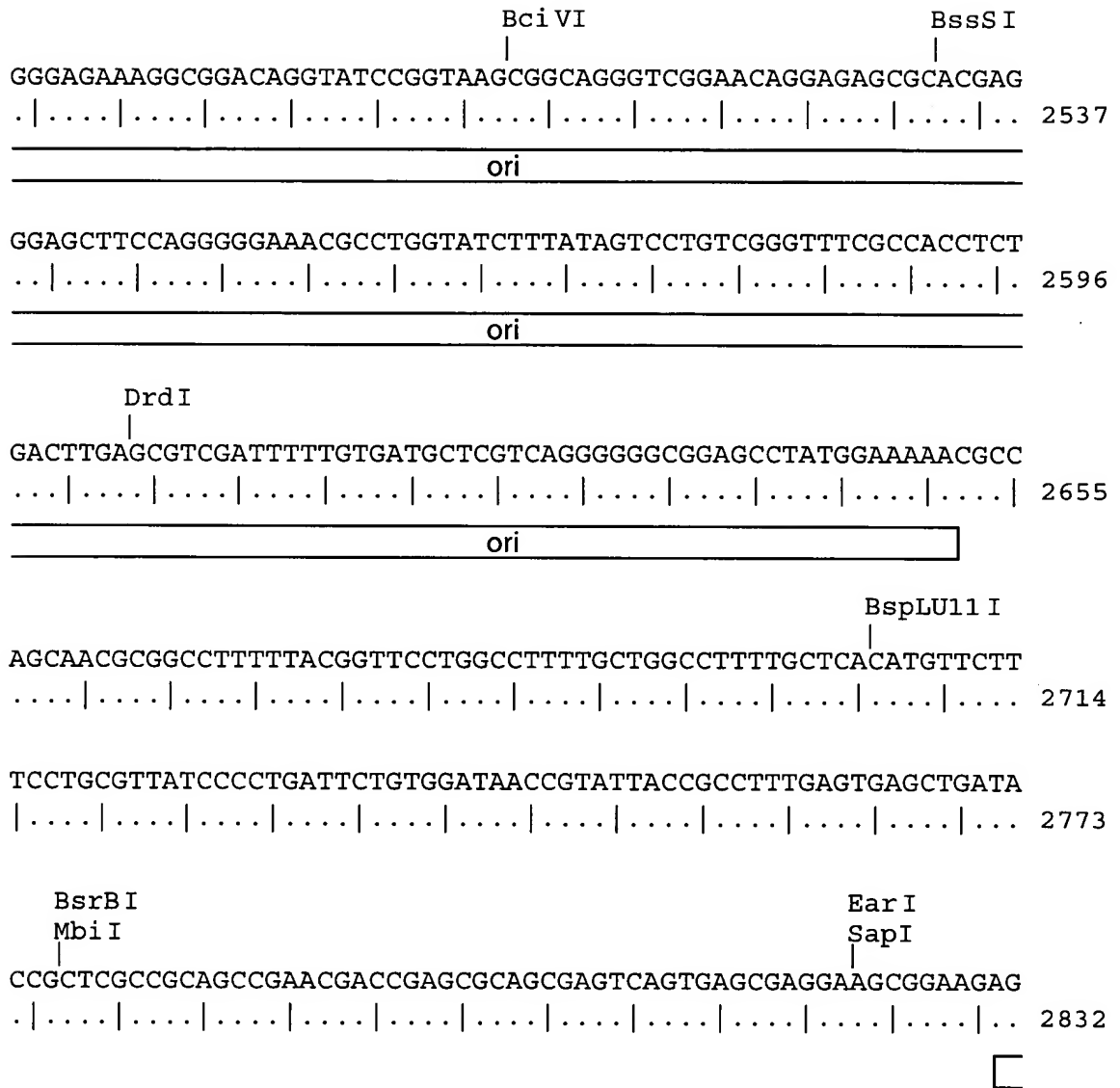


Fig. 4H

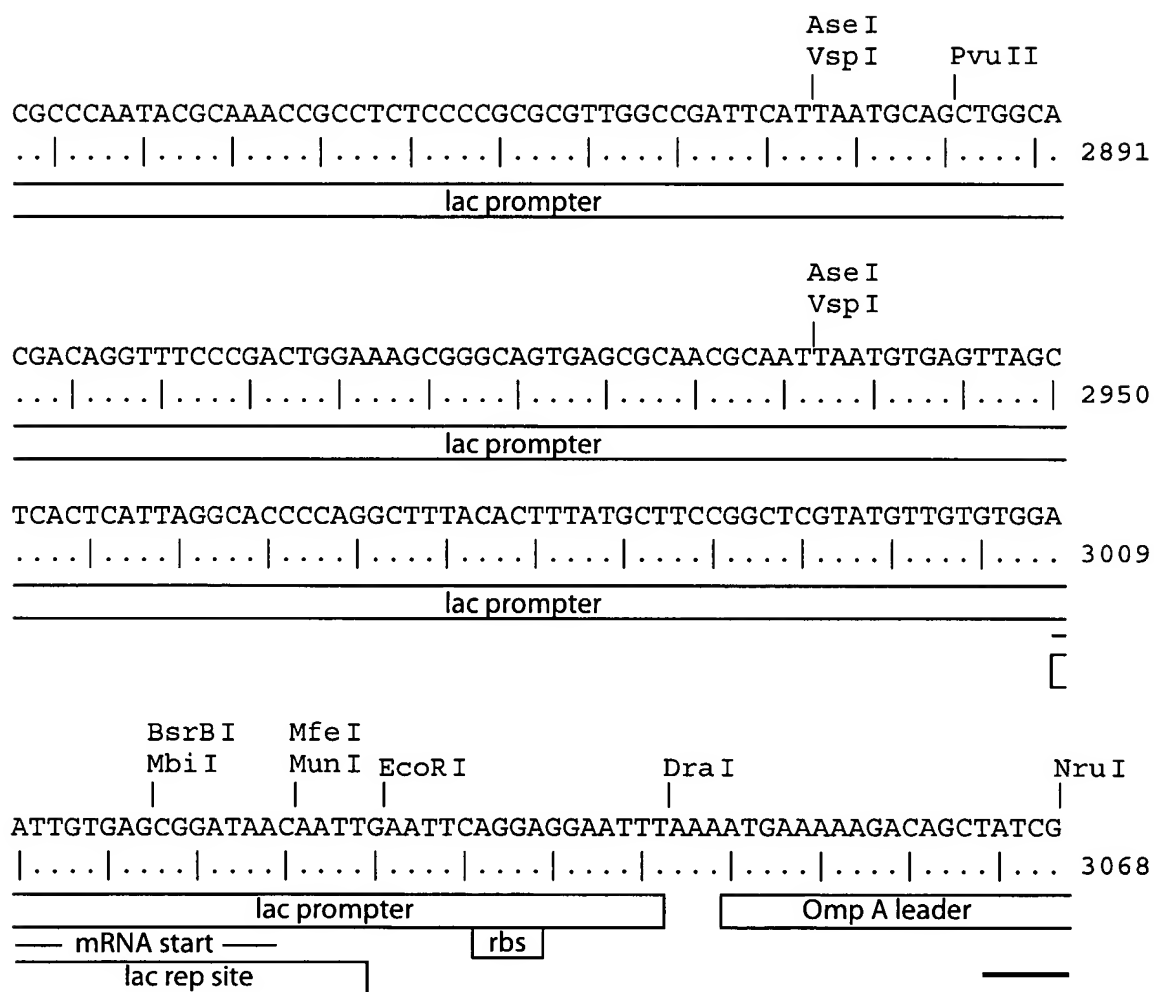


Fig. 4I

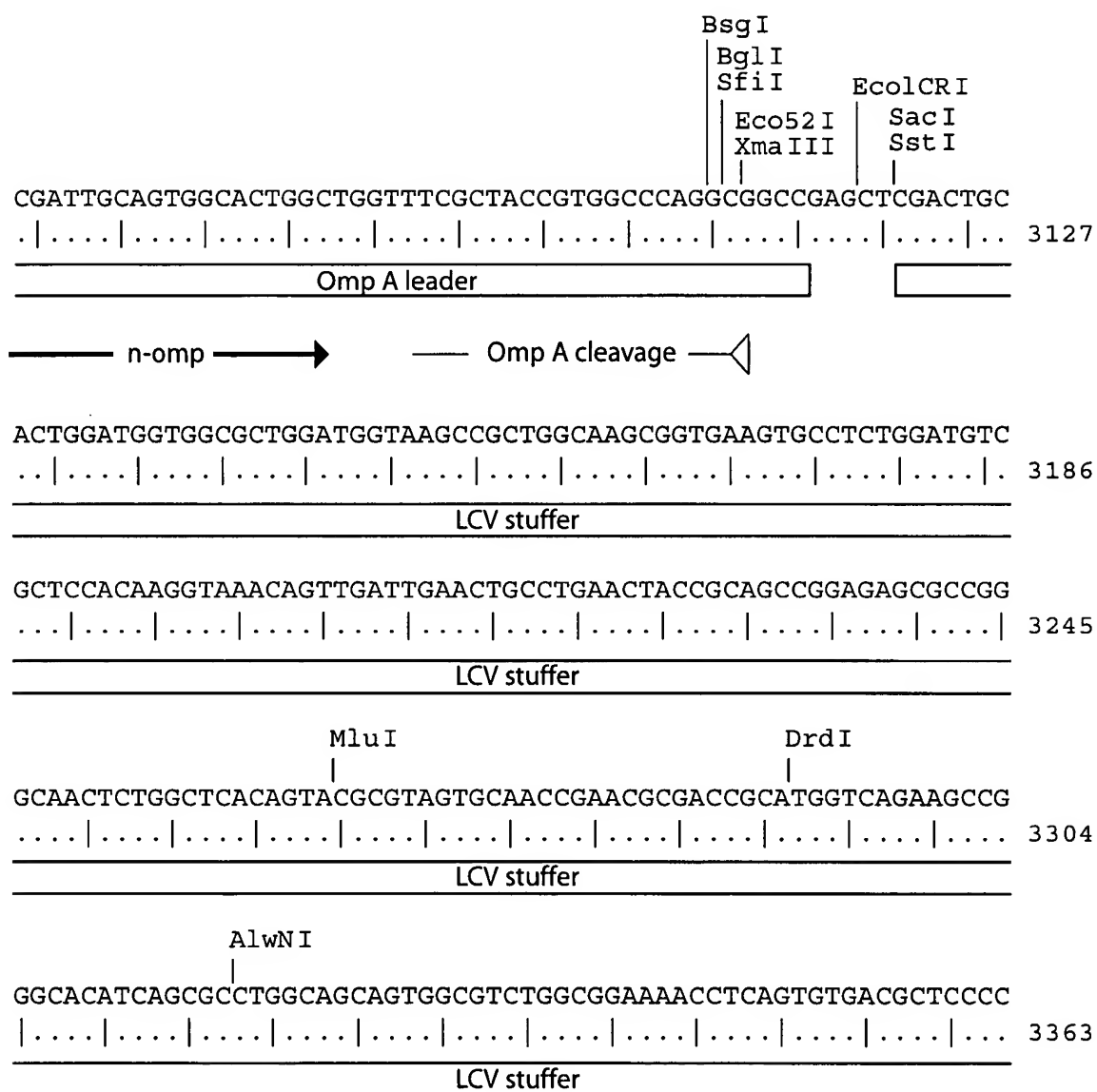


Fig.4J

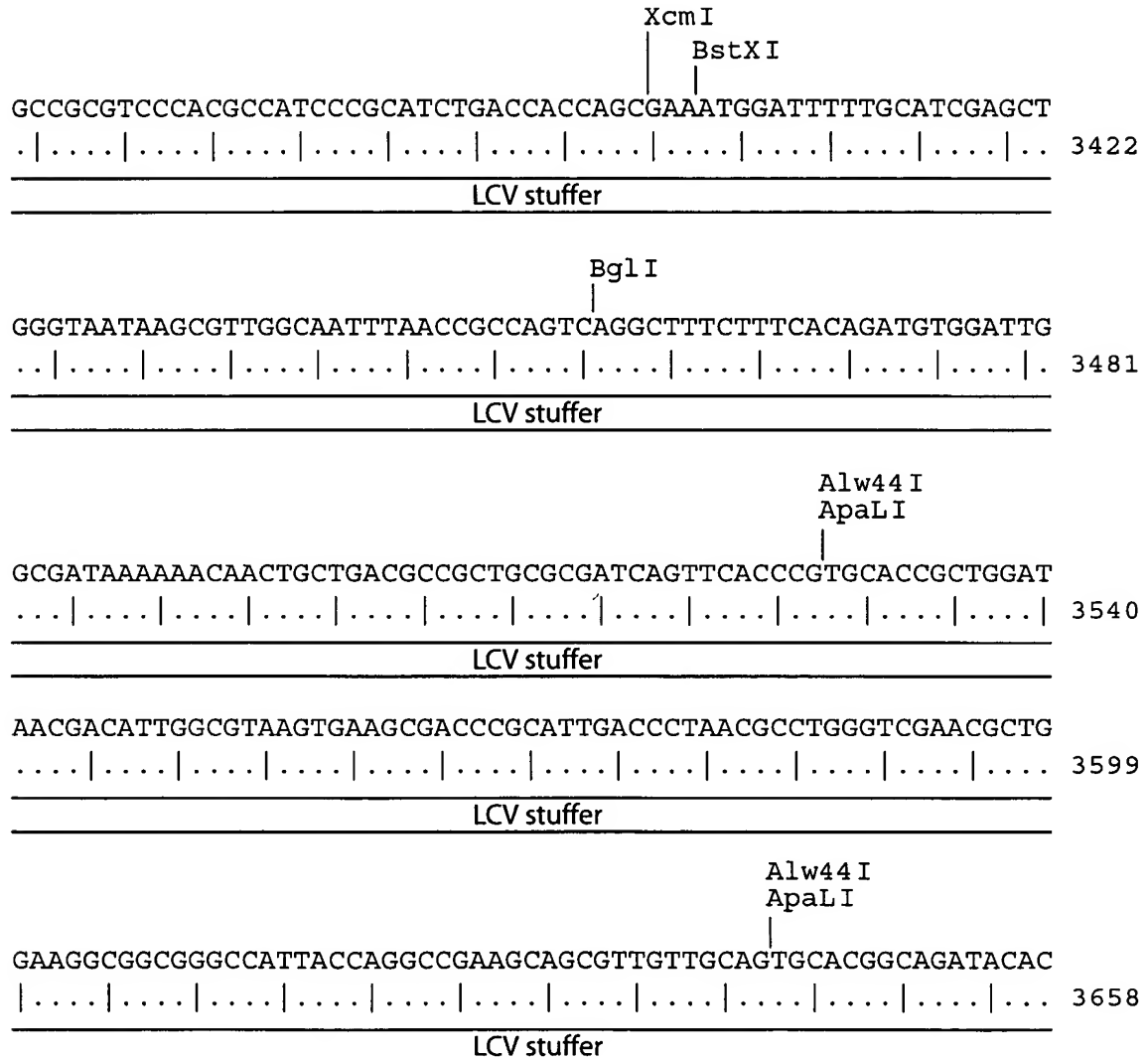


Fig. 4K

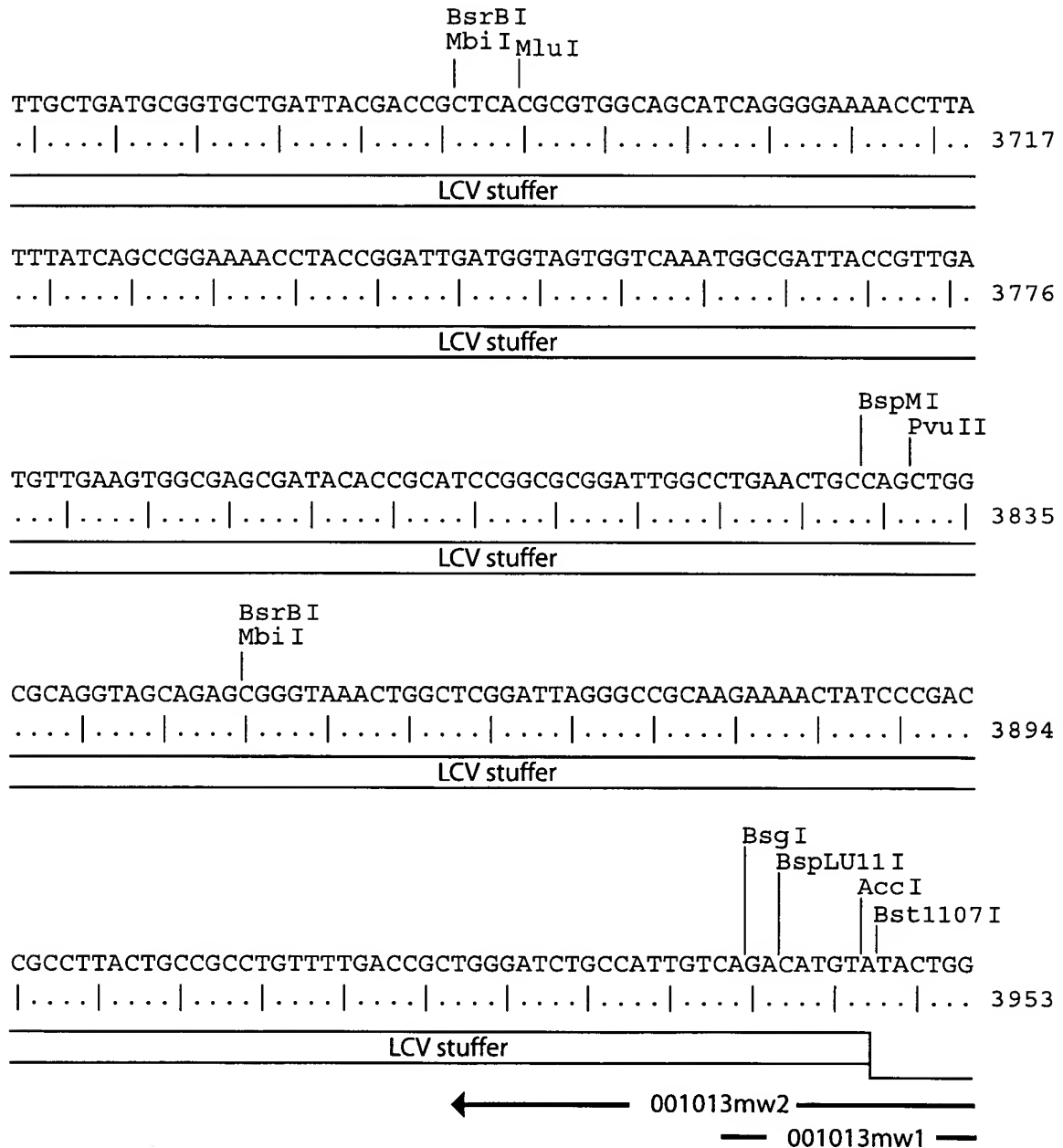


Fig. 4L

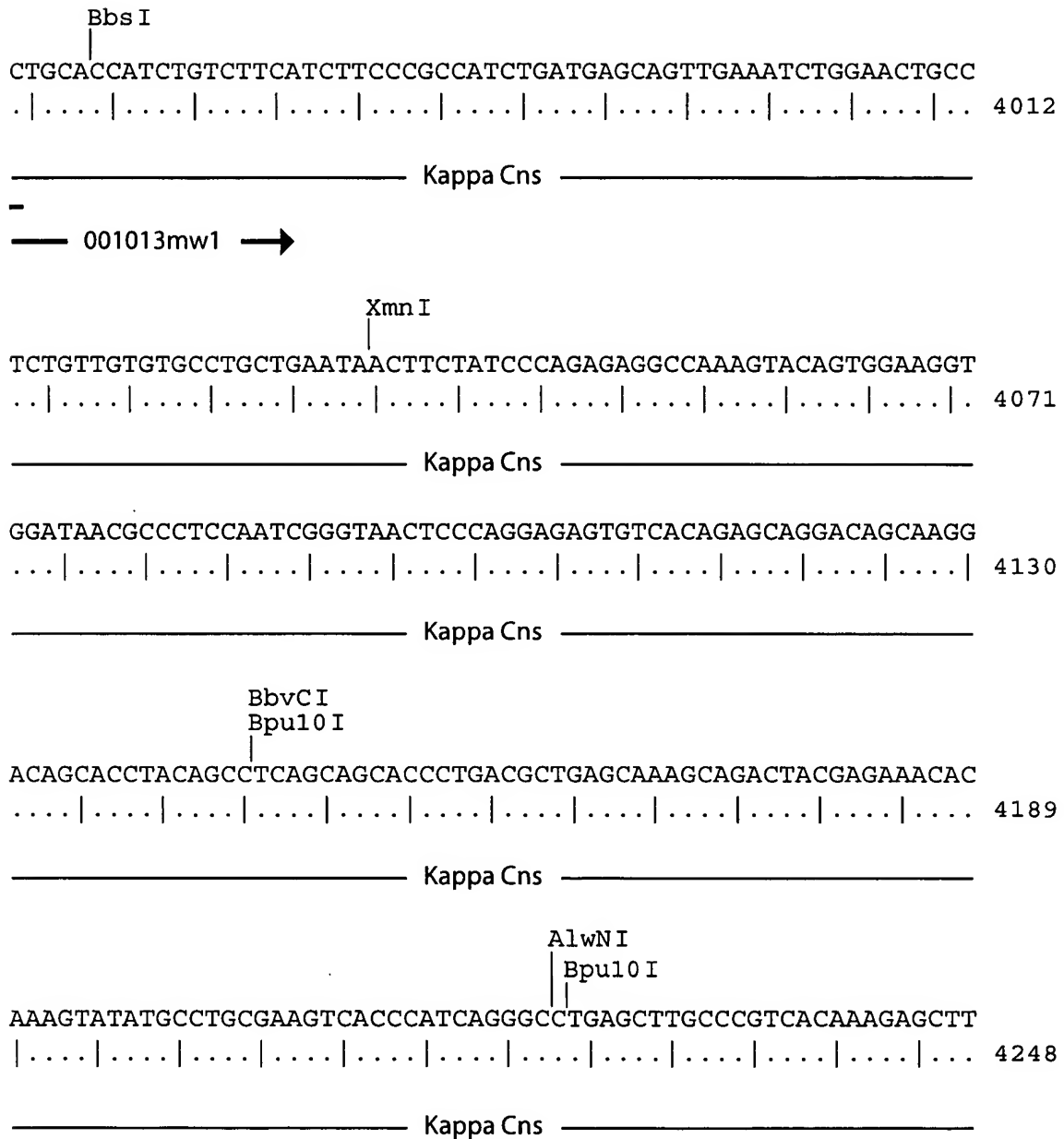


Fig. 4M

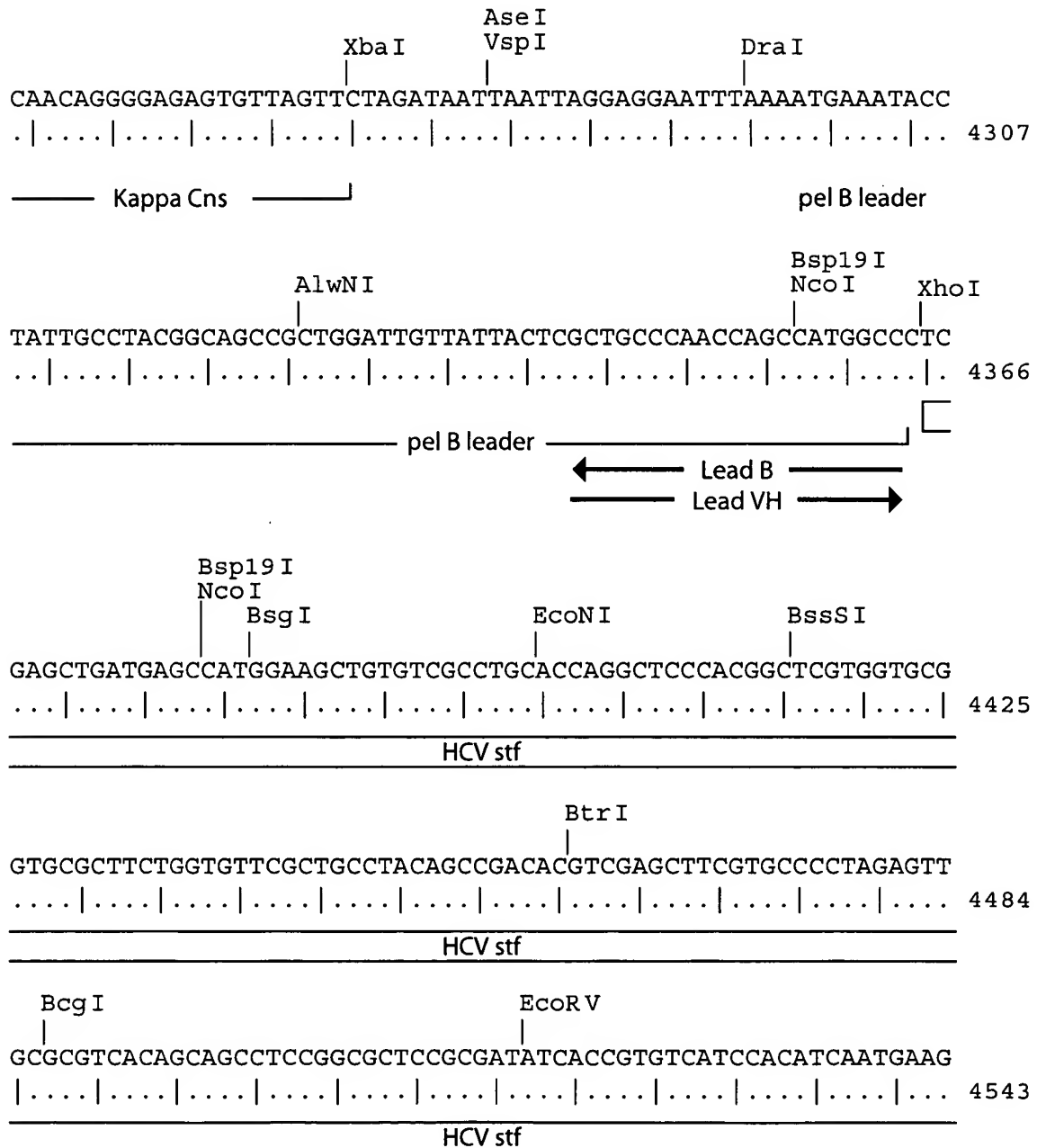


Fig. 4N

[illegible]

Fig. 40

[illegible]

Fig. 4P

BseR I
 CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
 ..|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. 5251
 EcoN I

Age I
 PinA I
 Tth111 I
 Kas I
 Nar I
 Ehe I
 Bbe I
 AGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCGGC
 ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. 5310

Alw44 I
 ApaL I
 Bsu36 I
 BbvC I
 Bpu10 I
 Bpm I
 BstE II
 GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. 5369

BstX I
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
 |. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. 5428

Bcu I
 Spe I
 Bcu I
 Bal I
 Msc I
 CCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAAGTACTAGTGGC
 .|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. ...|. 5487

└

Fig.4Q

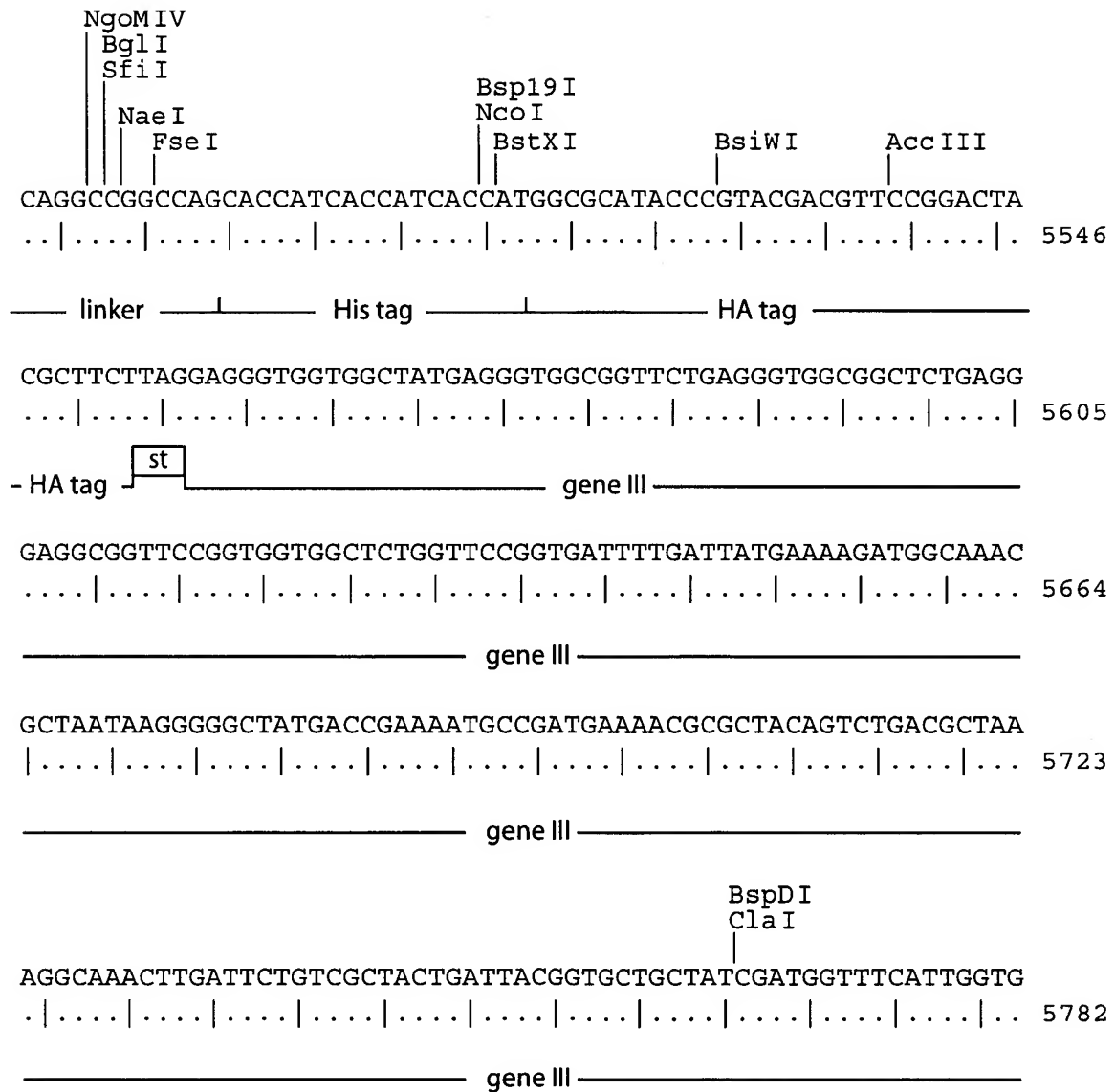


Fig. 4R

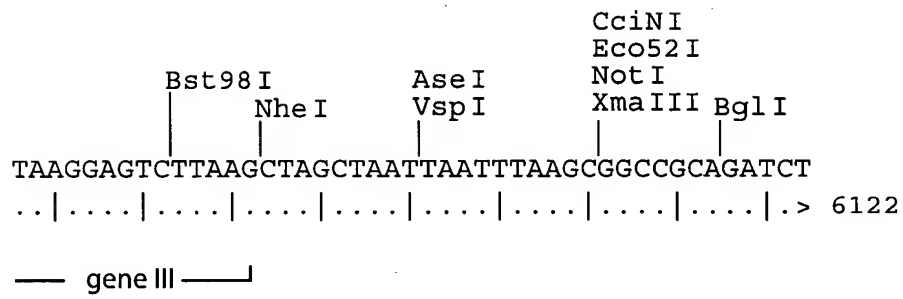


Fig. 4T

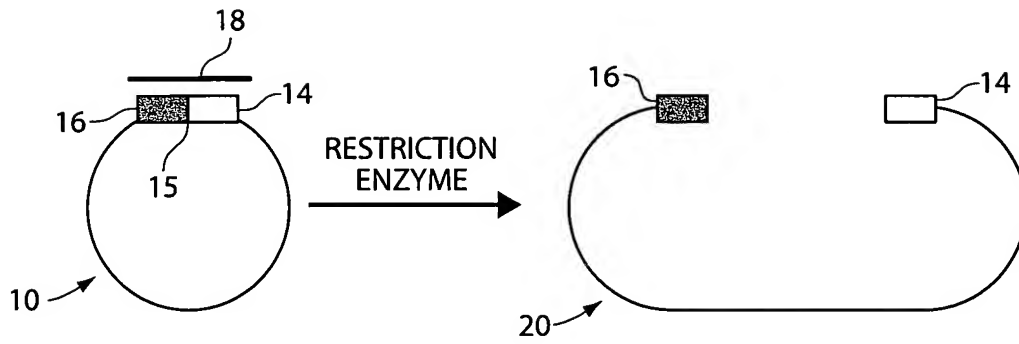


Fig. 5A

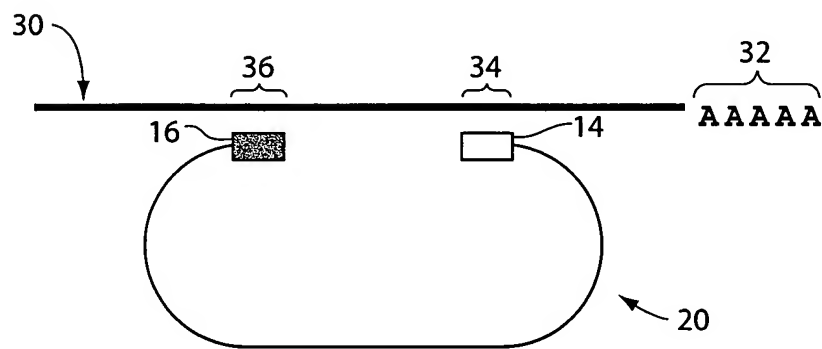


Fig. 5B

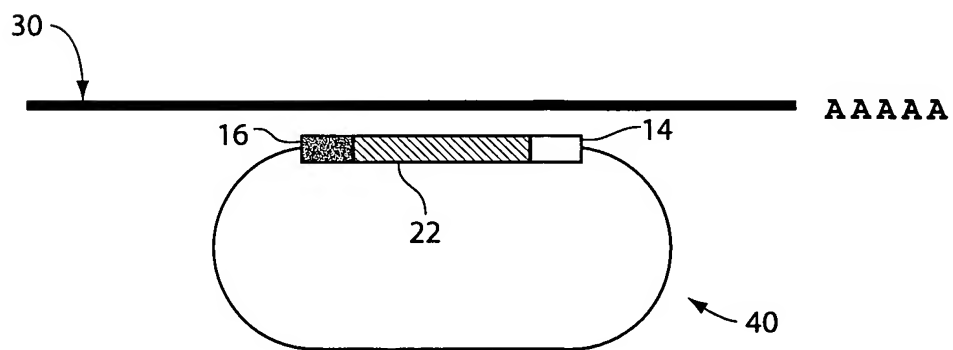


Fig. 5C

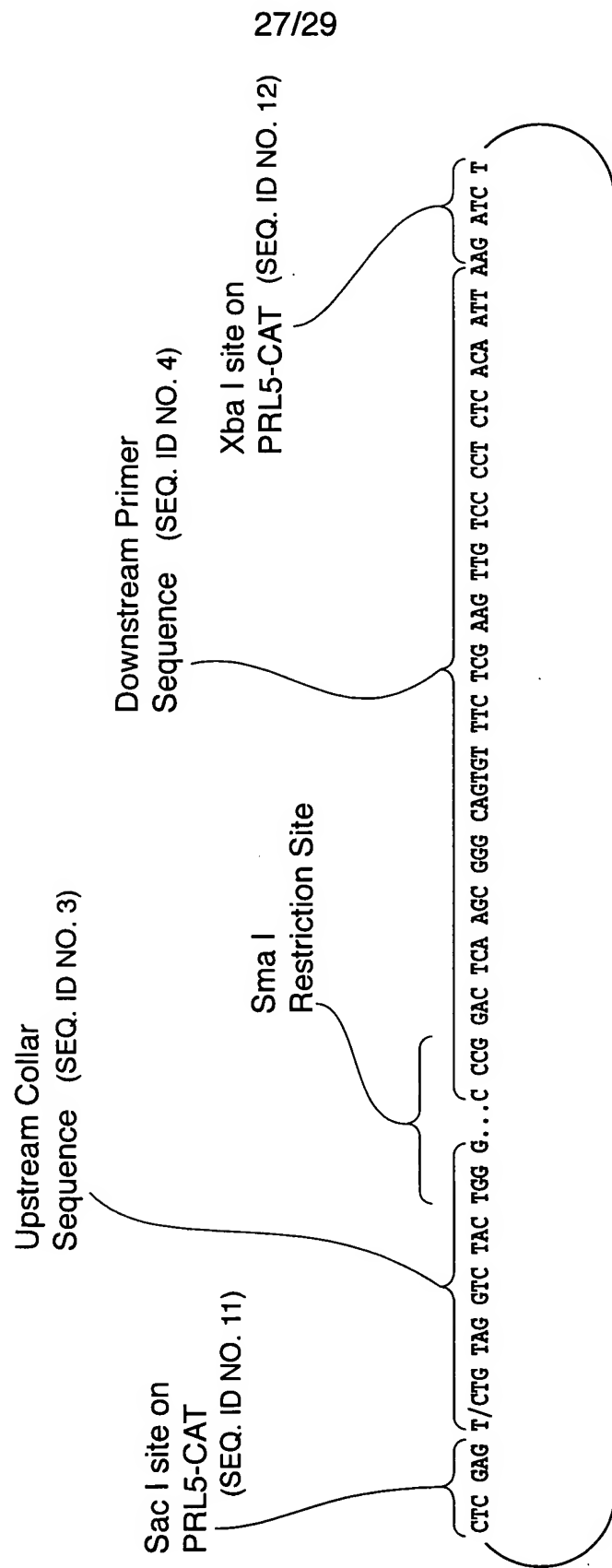


Fig. 6A

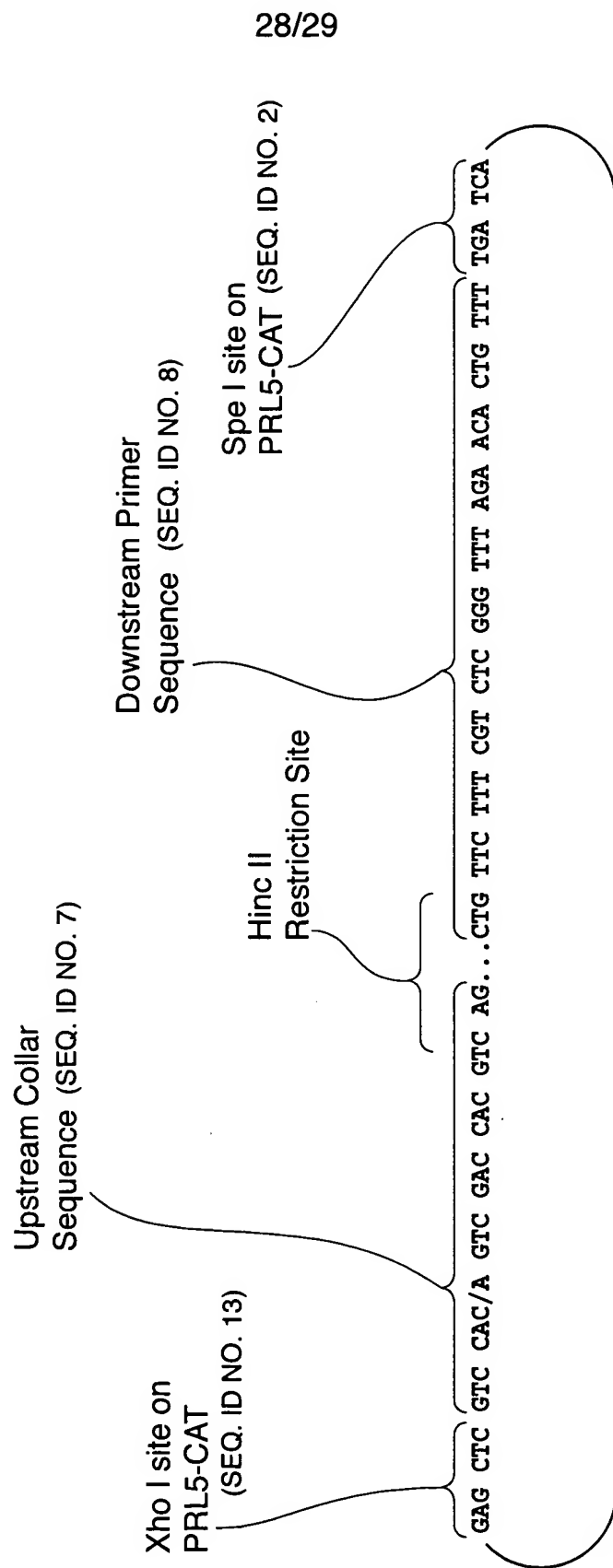


Fig.6B

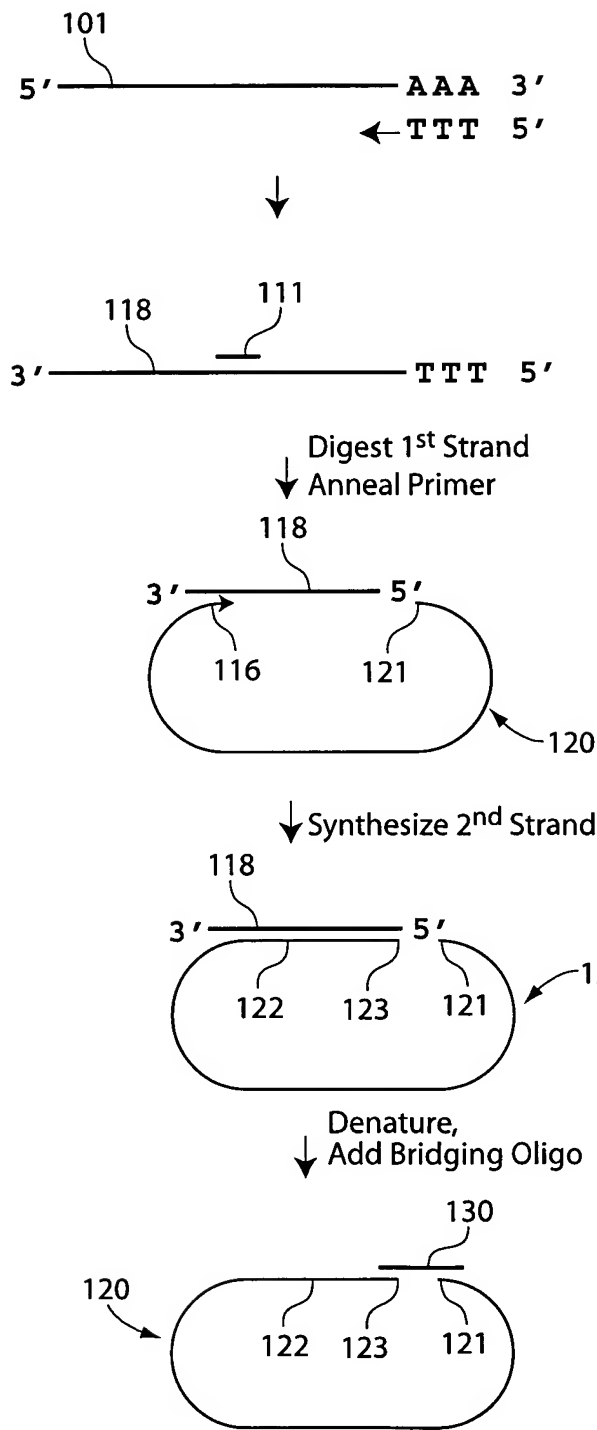


Fig. 7